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Maximum
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Query
Match
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| SIDS2/gcgdata/genesed/genesegp-emb1/AA2000.DAT:
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: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
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Copyright (c) 1993 - 2002 Compugen Ltd
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AAB02842
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ID AAY7
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28-MAY-1999;
28-MAY-1999;
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28-MAY-1999;
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26-FEB-1999;
12-MAR-1999;
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28-MAY-1999
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22323	22222	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	22222222222222222222222222222222222222
AAU10004 AAE17231 AAG77965 ABB05229	AAE07538 AAU04368 AAU07294 AAB73097 ABG66684	AAE204392 AAE01143 AAE01144 AAE071964 AAE07539 AAE12022 AAE12022	AAE04389 AAU10983 AAU10985 AAU04375 AAU04375 AAU04375 AAU04375 AAB83819 AAB83819 AAB83819 AAB83819 AAB83819 AAB83819 AAB83819 AAB83818 AAU77600 AA014027 AAE16171 AAE04390 AAB8375 AAG80971 AAB80375 AAG80971 AAB80991 AAB80991
Human CysLT2-like Human CysLT2 GPCR Human G-protein co Human LTD4-like G	el to	usculus GPC P2-puriner purinergic purinergic G-protein G-protein G-protein G-protein	

ALIGNMENTS

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Human; orphan G protein-coupled receptor; GPCR; hCHN10; drug screening; transmembrane receptor; expressed sequence tag; EST; signal cascade.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human orphan G protein-coupled receptor hCHN10
99US-0123949.
99US-0136436.
99US-0136437.
99US-0136439.
99US-0136439.
99US-0137127.
99US-0137127.
99US-0137131.
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99US-0120416.
99US-0121852.
99US-0123946.
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(first entry)

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Human, G protein coupled receptor; GPCR; transmembrane receptor;
identification; agonist; screening; therapeutic; pharmaceutical;
                                                                              Human G protein coupled receptor hCHN10 protein SEQ ID NO:38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Behan DP, Lehmann-Bruinsma K, Chalmers DT, (
Gore M, Liaw CW, Lin I, Lowitz K, White C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AREN-) ARENA PHARM INC.
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                                                                                                                                                                                                            WO200022131-A2.
                                                                                                                                                                               Homo sapiens.
                                               22-AUG-2000
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12-MAR-1999;
12-MAR-1999;
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28-MAY-1999;
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               AAB02842;
                                                                                                                                                 mutant.
·;
                                                                                                                                                                                                                                                                                                                                                                                                        orphan G protein-coupled receptor (GPCR), expressed in kidney and thyroid. The hCHNIO CDNA was identified using the human EST (expressed sequence tag) 1365839 as a probe. The orphan GPCR of the invention, like all GPCRs has seven transmembrane alpha helices with an extracellular N-terminus and an intracellular C-terminus. However, no endogenous ligands has yet been identified for the proteins of their endogenous orphan GPCRs may be used in the identification of their endogenous ligands, and to screen potential GPCR agonists and antagonists for use as pharmaceutical agents. The proteins may also be used in the study of GPCR-mediated signalling cascades, and to elucidate their precise role in normal and diseased human conditions. Nucleic acid encoding human orphan GPCRs may be used for tissue localisation expression analysis to provide information about their function in healthy and pathological states.
                                                                                                                                                                                                                                                                                                            the encoding cDNAs receptor agonists
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                            present amino acid sequence is the hCHN10, an endogenous human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YLIIKYPFREHLLQKKEFAILISLAIWVLVTLELLPILPLINPVITDNGTTCNDFASSGD
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0
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                                                                                                                                                                                                                                                                                                          Novel human orphan G protein-coupled receptors and for use in the identification of G protein-coupled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HFRDMLMNQLRHNFKSLTSFSRWAHELLLSFREK 334
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                                                                                                                                                                                                                                                                                                                                                            Claim 70; Page 87-88; 102pp; English.
                                                                                                                                                                                                                             Lin I;
                                          99US-0156653.
99US-0157280.
99US-0157281.
99US-0157282.
                                                                                                                                                                                                                          Dang HT, Liaw CW,
                                                                                                             99US-0157293.
99US-0157294.
99US-0416760.
           99US-0156633.
                                                                                                                                                             99US-0417044
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Matches 333; Conservative
                                                                                                                                                                                             PHARM INC
                                                                                                                                                                                                                                                            WPI; 2000-400068/34.
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                                                                                                                                                                                             (AREN-) ARENA
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12-OCT-1999;
             29-SEP-1999;
29-SEP-1999;
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Best Local 9
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98US-0109213 99US-0120416 99US-0121852

99US-0123949 99US-0136436 99US-0136439 99US-0137131 99US-0141448

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99US-0137567 99US-0151114

99US-0152524

99US-0156634

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99US-0137127

99US-0123946

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                                                                                                                                                                                                                                 human G protein coupled receptors (GPCR), for which the endogenous ligand is unknown (orphan GPCR receptors). More specifically the present invention relates to non-endogenous, constitutively activated versions of a human GPCR. These non-endogenous human GPCRs can be useful for the direct identification of candidate compounds as receptors agonists, inverse agonists or partial agonists for use as pharmaceutical agents. AAA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                 The present invention describes transmembrane receptors, preferably
Non-endogenous, human G protein-coupled receptors for screening receptor, inverse or partial agonists useful as therapeutic agents
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99.7%; Pred. No. 8.2e-172;
iive 0; Mismatches 1;
                                                                                                                          Example 1; Page 117-118; 187pp; English.
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Best Local Similarity 99.7
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AAB02842 standard; Protein; 334 AA

RESULT 2 AAB02842

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The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB89040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
                                                                                                                                                              gastrointestinal, disorders -
                                                                                                                                                                           Novel 1405 isolated polypeptides, useful for diagnosis, treatment prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human polypeptide SEQ ID NO
                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                   18-MAY-2001;
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                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME
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Best Local Simi
Matches 333;
                                                                                                                                                                                                                                                                                                                                                                                                                      Human; G-protein coupled receptor-3; GCREC-3; therapy; cancer; stroke; cell proliferative disorder; neurological; epilepsy; Parkinson's disease; Alzheimer's disease; inflammation; thyroiditis; haemolytic anaemia; AIDS; Acquired Immune Deficiency Syndrome; dementia; nootropic; cholelithiasis; multiple sclerosis; atherosclerosis; angina pectoris; gastroenteritis; diabetes; ulcer; viral infection; immunosuppressive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note: The sequence data for this patent did not form part printed specification, but was obtained in electronic form from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rune humatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human G-protein coupled receptor-3 (GCREC-3) protein.
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and parasitic infections.
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319..3
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                                                                                                                                                                                            label = Transmembrane_domain
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Pred. No. 8.2e-172;
0; Mismatches 1;
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P2U2 receptor; purinergic receptor; diagnosis; therapy
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/label= ECDIII
/note= "extracellular domain III"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= TMDVII
/note= "transmembrane domain VII"
                                                                                                                                                                                                                                                                                                                                                                                                   .00..119
|abel= TMIII
|note= "transmembrane domain III"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "intracellular domain III
                                                                                                                                                                                                                                                                                                                                                                                                                                           120..141
|Tabel= ICDII
|note= "intracellular domain II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [Jabel= TMDVI | Inote= "transmembrane domain VI"
                                                                                                                                                                                                                                                                                                                                                  note= "transmembrane domain II'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               label= ECDII
note= "extracellular domain II"
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                                                                                                                                                                                                                       ..23
label= N-terminal domain
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                                                                                                                                                                                                                                                                         note= "transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'label= TMDIV
'note= "transmembrane
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                                                 AAW19854 standard; Protein; 334 AA.
                                                                                                                            Human purinergic receptor P2U2.
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|abel= ICDI
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/label= TMII
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15-NOV-1995;
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                                    AAW19854
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                                                                                                                                                                                                                                                                                                                                                                     The invention relates to isolated human G-protein coupled receptor (GCREC) polypeptides and their biologically active fragments. GCREC and protein is useful in treating a disease or condition associated with an increase or decrease in expression of functional GCREC. The GCREC's are useful in the diagnosis, treatment and prevention of cell proliferative disorders (cancer, leukaemia, melanoma); neurological disorders (stroke, epilepsy, Parkinson's disease, dementia, Alzheimer's disease); autoimmune inflammatory disorder (thyroiditis, heemolytic anaemia, AIDS, multiple sclerosis); cardiovascular disorder (atherosclerosis, angina pectoris), metabolic disorders (diabetes); viral infections (herpes virus) and in the assessment of the effects of exogenous compounds on the expression of the multiple and amino acid sequences. The present sequence is
                                                                                                                                                                           Gandhi AR, Kallick DA,
Lu DAM, Tribouley CM;
Ramkumar J, Au-Young J;
iky ML, Thornton M, He A;
                                                                                                                                                                                                                                                                                  Isolated human G-protein coupled receptor polypeptides and the use of these sequences in the diagnosis, treatment and prevention of diseases and in the assessment of exogenous compounds on the expression of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180
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Pred. No. 9.7e-172;
0; Mismatches 1; Indels 0
                                                                                                                                                                            Baughn MR, Hafalia AJA, Nguyen DB, Gandh
in JA, Yue H, Khan FA, Patterson C, Lu DAM
walia NK, Graul R, Yoo MG, Yang J, Ramku
tt VS, Hernandez R, Walsh RT, Borowsky ML,
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                                                                                     07-JUL-2000; 2000US-216595P.
14-JUL-2000; 2000US-218936P.
19-JUL-2000; 2000US-219154P.
21-JUL-2000; 2000US-220141P.
                         15-JUN-2001; 2001WO-US19275.
                                                            2000US-213954P.
2000US-215209P.
                                                                                                                                                      (INCY-) INCYTE GENOMICS INC.
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Best Local Similarity 99.7
Matches 333; Conservative
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                                                            22-JUN-2000;
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Elliott VS,
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domain IV"

"transmembrane domain V"

domain I"

"intracellular domain I"

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ID AAW2
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Best Local S
Matches 331
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                                                                                                                                                                                                                                                      Human ATP receptor
  Misc-difference
                                                     Misc-difference
                                                                                                                                                                                              ATP receptor; G-protein coupled receptor; agonist; antagonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated purinergic receptor sub-type - used to develop products for diagnosis and therapy, e.g. for screening for agonists and antagonists which can modulate activation
                                                                                                                                                                                                                                                                                                                  07-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                       AAW22732;
                                                                                                                                                                                                                                                                                                                                                                                                                                AAW22732 standard;
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DB; AAT71900.
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/note= "encoded by TCC"
235
                                                        Location/Qualifiers 212
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Pred. No. 1.4e-170;
0; Mismatches 3;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human ATP receptor (AAW22732) is structurally related to the G protein-coupled receptor family. It shows 9.8% identity to a murine P2u receptor. Its amino acid sequence was deduced from a human placental cDNA clone (AAT75146). Recombinant ATP receptor can be expressed in bacterial (e.g. E. coli), mammalian (e.g. COS) or insect (e.g. Sf9) host cells and used to screen for agonists and antagonists useful in the treatment of conditions related to underexpression of the receptor (e.g. asthma, Parkinson's disease, acute heart failure, hypotension, urinary retention and osteoporosis) or underexpression of the receptor (e.g. arterial thrombosis, hypertension, thrombolysis, angioplasty, cystic fibrosis, ulcers, asthma, allergy, benign prostatic hypertrophy, psychotic and neurological disorders, dyskinesias, endogenous
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated human ATP receptor - agonists and antagonists of wuseful in treatment of, e.g. asthma, hypertension, arterial thrombosis and psychotic and neurological disorders
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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HFRDMLMNQLRHNFKSLTSFSRWAHELLLSFREK 334
                          HFRDMLMNQLRHNFKSLTSFSRWAHELLLSFREK 334
                                                      FSVXFTPYHVMRNVRIASRLGSWKQYQCTQVVINSFYIVTRPVAFLNSVINPVFYFLVGD
                                                                               FSVPFTPYHVMRNVRIASRLGSWKQYQCTQVVINSFYIVTRPLAFLNSVINPVFYFLLGD
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                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                      334 AA;
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244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "encoded
                                                                                                                                                                                                                                                                                                                                                           Score 1721; DB 18;
Pred. No. 3.7e-170;
3; Mismatches 2;
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RESULT

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The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a diesase associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a parhology related to abstrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and the proteins are useful as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU25910-AAU33304 represent the amino acid sequences of novel human secreted proteins of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SVSDLAFLCTLPMLIRSYANGNWIYGDVLCISNRYVLHANLYTSILFLTFISIDRYLIIK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 YPFREHLLQKKEFAILISLAIWVLVTLELLPILPLINPVITDNGTTCNDFASSGDPNYNL 185
                                                                                                                                                              Human, vaccination, gene therapy, nutritional supplement,
stem cell proliferation, haematopoiesis, nerve tissue regeneration,
immune suppression, immune stimulation, anti-inflammatory, leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179 YPFREHLLOKKEFALLISLAIWULVTLELLPILPLINPVITDNGTTCNDFASSGDPNYNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 AWNATCKNWLAAEAALEKYYLSIFYGIEFVVGVLGNTIVVYGYIFSLKNWNSSNIYLFNL
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Pred. No. 1.8e-167;
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                                                                                                                            protein #1520.
                    AAU31029 standard; Protein; 387 AA
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98.8%;
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26-JAN-2001; 2001US-0770160.
                                                                                          (first entry)
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                                                                                                                              Novel human secreted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rang YT, Liu C,
                                                                                                                                                                                                                                                                          WO200179449-A2.
                                                                                                                                                                                                                                          Homo sapiens.
                                                                                          18-DEC-2001
                                                                                                                                                                                                                                                                                                              25-OCT-2001
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                                                      AAU31029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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AAU31029
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The polynucleotide sequences given in AAC81086 to AAC81134 encode the human secreted proteins given in AAB45308 to AAB45355. AAB45357 to AAB45384 represent human secreted polypeptide sequences and proteins homologous to them, which are given in the exemplification of the present invention. Human secreted proteins have activities based on the tissues and cells the genes are expressed in. Examples of activities include: antiarthritic; immunosuppressive; antirhematic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; chromities and polypeptides can be used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, cabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or susceptibility to a cutoimmune diseases, hyperproliferative disonosed or treated include autoimmune diseases, hyperproliferative disonoses, nervous system disorders, cerebrovascular disorders, angiogenesis, nervous system disorders, infections caused by bacteria, viruse; and fungi and ocular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; ophthalmological; vulnerary; gene therapy; autoimmune disease; hyperproliferative disorder; cardiovascular disorder; angiogenesis; cerebrovascular disorder; nervous system disorder; infection; skin aging; ocular disorder; wound healing; food additive; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid molecules encoding 49 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      culture of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disorders. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, tamintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate Lissues and in chemotaxis. The
239 IYSMCLTLLGFSIPLFVMCLFYYKIALFLKQRNRQVATALPLEKPLNLVIMAVVIFSVLF 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, secreted protein, diagnosis, immunosuppressive, antiarthritic,
                                                                       299 TPYHVMRNVRIASRIGSWKQYQCTQVVINSFYIVTRPLAFINSVINPVFYFLLGDHFRDM
                                               TPYHVMRNVRIASRLGSWKQYQCTQVVINSFYIVTRPLAFLNSVINPVFYFLLGDHFRDM
                                                                                                                                                                                                                                                                                                                                                                                                                                     Human secreted protein sequence encoded by gene 37 SEQ ID NO:128.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 447-448; 454pp; English.
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                                                                                                                                                                LMNOLRHNFKSLTSFSRWAHELLLSFREK 387
                                                                                                                                      LMNQLRHNFKSLTSFSRWAHELLLSFREK 334
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14-JAN-2000; 2000US-0176052.
                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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Best Local Similarity
                                                                                                       New G-protein coupled receptor polypeptides, useful for identifying modulators of signal transduction for treating kidney disease, hyperlipidemia, obesity, dyslexia and cardiac myxoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse; G-protein coupled; receptor; GPCR; TGR18; kidney disease; signal transduction modulator; cerebral cavernous malformation; hyperlipidemia; obesity; dyslexia; cardiac myxoma; renal failure; nephritis; hypertension; liver disease; cirrhosis; blood disorder
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                                                     Claim 33; Page 59; 78pp; English
                                                                                                                                                                                                                                                                                                                                                                                                        23-JUN-2000; 2000US-213461P
                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-JUN-2001; 2001WO-US20363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-APR-2002
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                                                                                                                                                                                                                                                                                                                                                     (TULA-)
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)B; ABK12957.
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                                                                                                                                                                                                                                                                                                                                                     TULARIK INC.
                                                                                                                                                                                                                                                                                                Zhao J,
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                                                                                                                                                                                                                                                                                                Chen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein; 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                258
                                                                                                                                                                                                                                                                                                   Cutler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immune disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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Pred. No. 5.2e-130;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    203
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present invention relates to a new G-protein coupled receptor (GPCR)

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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC polypeptide comprising greater than 70% amino acid sequence identity to CC the amino acid sequence of human GPCRS TGR62, TGR21, TGR230.2, TGR2130.2, TGR230.2 TGR22, 80% amino acid sequence identity to mouse TGR18 CC or 90% amino acid sequence identity to human novel edg receptor protein, CC as defined in the specification. The GPCR covalently linked to a solid CC phase is useful for identifying a compound that modulates signal CC transduction. The identified compounds are useful for treating CC kidney disease, cerebral cavernous malformations, hyperlipidemia, CC which the compound that modulates signal CC cobsistry, dyslexia and cardiac myxoma. The molecules of the invention are useful for diagnosing disorders or conditions such as kidney-related CC conditions or diseases such as renal failure, nephritis, nephrotic CC syndrome, asymptomatic urinary abnormalities, renal tubule defects, CC hypertension and nephrolithiasis, liver-related disorders and jaundice e.g. cirrhosis, infiltrations, lesions, functional disorders and jaundice CC and spleen-associated disorders or conditions e.g. splenic enlargement, CC immune disorders, blood disorders and others. Modulation of the CC above conditions or diseases. The present amino acid sequence represents the mouse GPCR TGR18 protein of the invention. This sequence is one of CC analyzation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 227
                                                                                                                     Purinergic receptor P2Y, G-protein coupled 1; coagulant; platelet aggregation; haplotyping; transgenic animal; human.
                                 Misc-difference
                                                                                    Homo
                                                                                                                                                                                       Purinergic receptor
                                                                                                                                                                                                                              12-MAR-2002
                                                                                                                                                                                                                                                                                                AAU10984 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                               AAU10984;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 MAWNATCKWWLAAEAALEKYYLSIFYGIEFVVGVLGNTIVVYGYIFSLKWWNSSNIYLFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  μ.
                                                                                                                                                                                                                                                                                                                                                                                                                        MLMNQLRHNFKSLTSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FTPYHVMRNVRIASRLGSWKQYQCTQVVINSFYIVTRPLAFLNSVINPVFYFLLGDHFRD 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KYPFREHLLQKKEFAILISLAIWVLVTLELLPILPLINPVITDNGTTCNDFASSGDENYN 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSVSDLAFLCTLPMLIRSYANGNWIYGDVLCISNRYVLHANLYTSILFLTFISIDRYLII 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAQNLSCENWLATEAILNKYYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFN
                                                                                  sapiens
                                                                                                                                                                                                                                                                                                                                                                                     MLISKFRQYFKSLTSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIYSLCLTLLGFLIPLSVMCFFYYKMVVFLKRRSQQQATALPLDKPQRLVVLAVVIFSIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIYSMCLTLLGFLIPLFVMCFFYYKIALFLKQRNRQVATALPLEKPLNLVIMAVVIFSVP 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KYPFREHFLOKKEFAILISLAVWALVTLEVLPMLTFINSVPKEEGSNCIDYASSGNPEHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSISDFAFLCTLPILIKSYANDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                           FTPYHIMRNLRIASRLDSWPQ-GCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 71.8
27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            317 AA;
                                                                                                                                                                                                                          (first
                                                 Location/Qualifiers
                                                                                                                                                                                           P2Y,
                                                                                                                                                                                                                          entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70.5%;
71.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                         320
            "Wild type Ala
                                                                                                                                                                                       G-protein coupled 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42;
                                                                                                                                                                                                                                                                                                  373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1231.5; DB 2
Pred. No. 2.4e-119;
12; Mismatches 46;
                                                                                                                                                                                                                                                                                                  B
              substituted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46;
                                                                                                                                    P2RY1; anticoagulant; drug screening;
                                                                                                                                                                                           isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23;
              γď
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                                                                                                                                                                                           #1.
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel isolated polypeptide comprising a sequence which is a polymorphic variant of a reference sequence for the sequence which is a polymorphic variant coupled, I (PZRYI) protein or its fragment. The polymorphic variant comprises one or more variant amino acids selected from valine at a position 34 and glycine at a position 25c. The polymorphic variants are useful in studying the expression and function of PZRYI, in expressing PZRYI protein for use in screening for candidate drugs to treat diseases related to PZRYI activity, in studying the effect of the variation on the biological activity of PZRYI, and the binding affinity of candidate drugs targeting PZRYI for the treatment of disorders related to platelet aggregation. The halotyping methods are useful in validating PZRYI as a candidate to associated with PZRYI activity, or in the design of clinical trials of candidate drugs for treating a specific condition or disease associated with PZRYI activity, or in the design of clinical trials of expression of the PZRYI isogenes in vivo, for in vivo screening and testing of the PZRYI activity, or in the design of clinical trials of expression of the PZRYI isogenes in vivo, for in vivo screening and testing of therapeutic agents and compounds for disorders related to platelet aggregation in a biological system. The present sequence represents the amino acid sequence of human purinergic receptor PZY, and according the according a pacing the according and compounds for disorders related to presents the amino acid sequence of human purinergic receptor PZY, and according the according according the according and according to the pace to the pace the according to the pace the pac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G-coupled protein 1 (P2RY1), isoform #1.
Note: This sequence is not shown in the specification but is
derived from the human wild type P2RY1 sequence given in Figure 3 (see
                                                                                                                                                                                                                                                                                                                 New purinergic receptor P2Y G-protein coupled 1 (P2RY1) gene polyworphic variants, useful e.g. in studying the expression and function of P2RX1 and screening candidate drugs for treating diseases related to P2RX1 activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 NSSNIYLFNLSVSDLAFLCTLPMLIRSYAN-GNWIYGDVLCISNRYVLHANLYTSILFLT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FISIDRYLIIKYPFREHLLQKKEFAILISLAIWVLVTLELLPILPLINPVITDNGT-TCN 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 AW-NATCKNWLAA----EAALEK----YYLSIFYGIEFVVGVLGNTIVVYGYIFSLKNW 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 SWGNSTVASTVAVSSSFKCALTKTGFQFYYLPAVYILVFIIGFLGNSVAIWMFVFHMKPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DFASSGDPNYNLIYSMCLTLLGFLIPLFVM--CFFYYKIALFLKORNROVATALPL-EKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LNLVIMAVVIFSVPFTPYHVMRNVRIASRLGSWKQYQCT-QVVINSFYIVTRPLAFLNSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 499.5; DB 23; Length Pred. No. 3.1e-43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page -; 79pp; English.
                                                                                                                                                                                                                              Tanguay DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , 61 ;
                                                                                                                                                                               (GENA-) GENAISSANCE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.6%;
36.3%;
                                                                                         21-MAY-2001; 2001WO-US16432.
                                                                                                                                    19-MAY-2000; 2000US-205996P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                              Koshy B,
                                                                                                                                                                                                                                                                      WPI; 2002-083074/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   373 AA;
WO200190117-A2
                                            29-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 117;
                                                                                                                                                                                                                            Kazemi A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU10983)
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Human; P2-purinergic receptor; P2Y1; cardiant; vasotropic; thrombolytic; cerebroprotective; gynaecological; ADP; adenosine 5'-diphosphare; angina; myocardial infarction; ischaemic attack; preeclampsia; bleeding disorder; carotid endarterectomy; vascular graft surgery; brain disorder; migraine; vascular injury; schizophrenia; eating disorder; depression; angioplasty; peripheral vascular disease; platelet aggregation; restenotic; embolism; thrombocytopaenic purpura; stroke; pertussis toxin-sensitive G protein; disseminated intravascular coagulation; thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to ADP (adenosine 5'-diphosphate) receptor, termed as P2Y12 receptor and its corresponding cDNA molecule. P2Y12 receptor is the subtype of P2-purinegic receptor. The P2Y12 receptor is expressed selectively in the platelets and brain, and couples to a pertuasis toxinsensitive G protein (Gi). P2Y12 receptor is a G protein-coupled receptor identifying an agent which is useful for modulating acute myocardial infarction, unstable angina, chronic stable angina, transient ischaemic attacks, strokee, peripheral vascular disease, precolampsia, deep venous thrombosis, embolism, disseminated intravascular coagulation, thrombotic thrombocytopaenic purpura or a bleeding disorder; thrombotic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   useful
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for identifying binding partners and for diagnostic applications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Julius DJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3..76
label= Transmembrane_domain_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         label= Transmembrane_domain_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      label= Transmembrane_domain_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       label= Transmembrane domain 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58..283
label= Transmembrane_domain_6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 label= Transmembrane_domain_7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transmembrane domain 4
                                                                                                                                                                                                                                                                                                                                                                                                                          P2-purinergic receptor subtype, P2Y1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                               AAE04389 standard; Protein; 373 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure, Fig 5A; 108pp, English.
                                        319 VDPILYFLAGDTFRRLSRATR 340
290 INPVFYFLLGDHFRDMLMNQLR 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CORT-) COR THERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-DEC-2000; 2000WO-US34998.
                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24..148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17..241
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Best Local Sim.
Matches 117;
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                                                                                                              Kazemi A,
                                                                                                                                                                                                                                  19-MAY-2000; 2000US-205996P
                                                                                                                                                                                                                                                                                            21-MAY-2001; 2001WO-US16432
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                                                                                                                                                                              GENAISSANCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor P2Y, G-protein coupled 1; platelet aggregation; haplotyping; animal; human.
                                                                                                                 Koshy B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               373 AA;
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                                                                                                                                                                              PHARM INC
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                                                                                                                 Tanguay DA;
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Pred. No. 5e-43;
0; Mismatches 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P2RY1; anticoagulant; drug screening;
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PT New purinergic receptor P2Y G-protein coupled 1 (P2RY1) gene polymorphic variants, useful e.g. in studying the expression and pr function of P2RY1 and screening candidate drugs for treating diseases PT related to P2RY1 activity - XX

Claim 28; Fig 3; 79pp; English.

CC The invention relates to a novel isolated polypeptide comprising a comprise which is a polymorphic variant of a reference sequence for the foreign creceptor P2Y, G-protein coupled, 1 (P2RY1) protein or its creaming to receptor P2Y, G-protein coupled, 1 (P2RY1) protein or its creaming to polymorphic variant comprises one or more variant amino compared to the polymorphic variant comprises one or more variant amino compared to the polymorphic variants are useful in studying the expression compared to the polymorphic variants are useful in studying the expression compared to the polymorphic variant on the biological activity of condition of the polymorphic variation on the biological activity of conditions and the binding affinity of candidated to p2RY1 activity of candidated to p2RY1 as a candidate compared to treatment of disorders related to platelet aggregation. The condition or disease predicted to be cappet for treating a specific condition or disease predicted to be cappet for treating a specific condition or disease associated with P2RY1 activity, or in the design of clinical trials of candidate drugs targeted against p2RY1 protein, and for testing the testing of drugs targeted against p2RY1 protein, and for testing the ceptor p2RY1 activity. The transgenic animals are useful for studying candidate the passed to passed the passed to passed the passed to pas
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밁 á 밁 δ 밁 á á δ 밁 В á Matches Query Match Best Local : 290 259 204 174 144 Local 84 24 6 AW-NATCKNWLAA----EAALEK-----YYLSIFYGIEFVVGVLGNTIVVYGYIFSLKNW INPVFYFLLGDHFRDMLMNQLR : |||: : :|:| : |:|||: : : :|| IYLVIIVLTVFAVSYIPFHVMKTMNLRARLDFQTPAMCAFNDRVYATYQVTRGLASLNSC 318 LNLVIMAVVIFSVPFTPYHVMRNVRIASRLGSWKQYQCT-QVVINSFYIVTRPLAFLNSV CISAHRYSGVVYPLKSLGRLKKKNAICISVLVWLIVVVAISPILFYSGTGVRKNKTITCY FISIDRYLIIKYPFREHLLQKKEFAILISLAIWVLVTLELLPILPLINPVITDNGT-TCN 173 NSSNIYLFNLSVSDLAFLCTLPMLIRSYAN-GNWIYGDVLCISNRYVLHANLYTSILFLT 114 SWGNSTVASTAAVSSSFKCALTKTGFQFYYLPAVYILVFIIGFLGNSVAIWMFVFHMKPW DFASSGDPNYNLIYSMCLTLLGFLIPLFVM--CFFYYKIALFLKQRNRQVATALPL-EKP SGISVYMENLALADELYVLTLPALIFYYENKTDWIFGDAMCKLQRFIFHVNLYGSILFLT DTTSDEYLRSYFIYSMCTTVAMFCVPLVLILGCYGLIVRALIYKDLDNS-----PLRRKS Similarity Conservative 28.5%; 60; 311 Score 497.5; DB Pred. No. 5e-43; Mismatches DB 23; 124; Indels Length 373; 21; Gaps 289 55 258 203 83

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VDPILYFLAGDTFRRRLSRATR 340

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receptors for direct identification of candidate compounds as agonists, inverse agonists or partial agonists for use as therapeutic agents
DFASSGDPNYNLIYSMCLTLLGFLIPLFVM---CFFYYKIALFLKQRNRQVATALPL-EKP 230
                                                                                                                  The sequence represents a human G-protein coupled receptor (GPCR), hRUP21. The endogenous and non-endogenous, constitutively activated versions of human G-protein coupled receptors (GPCR), are useful for direct identification of candidate compounds as receptor agonists,
                      231 INLVIMAVVIESVPFTPYHVMRNVRIASRLGSWKQYQCT-QVVINSFYIVTRPLAFLNSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Endogenous and non-endogenous versions of human G-protein coupled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G-protein coupled receptor; GPCR; hRUP21; agonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human G-protein coupled receptor, hRUP21.
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                                                                                                                                                                                                                                                                                                                                 AAU04375 standard; Protein; 337 AA.
                                                                                                                                                                           290 INPVFYFLLGDHFRDMLMNQLR 311
                                                                                                                                                                                                      inverse agonist; lung cancer.
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99US-0171900.
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2000US-0196078
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14-MAR-2000;
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10-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                        23-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAY-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                             AAU04375;
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                                                                                                                                                                                                                                                                                        RESULT 14
AAU04375
  174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invanion relates to a movel isolated polypepties compliance of the invanion relates to a movel isolated by pepties compliating a golymorphic variant of a reference sequence for the purinergic receptor P2Y, G-protein coupled, I (P2RYI) protein or its fragment. The polymorphic variant comprises one or more variant amino acids selected from valine at a position 34 and glycine at a position 262. The polymorphic variants are useful in studying the expression of P2RYI in expressing P2RYI protein for use in screening for candidate drugs to rreat diseases related to P2RYI activity, in studying the effect of the variation on the biological activity of P2RYI, and the binding affinity of candidated to P2RYI activity, or the treatment of disorders related to platelet aggregation. The haplotyping methods are useful in validating P2RYI as a candidate treatment of disorders related to observe the treatment of disorders are useful in validating P2RYI activity. The transgenic animals are useful for studying expression of the P2RYI activity, or in the design of clinical trials of candidate drugs for treating a specific condition or disease associated with P2RYI activity. The transgenic animals are useful for studying expression of the P2RYI isogenes in vivo, for in vivo screening and esting of drugs targeted against P2RYI protein, and for testing the efficacy of therapeutic agents and compounds for disorders related to platelet aggregation in a biological system. The present sequence from the human wild type P2RYI sequence given in Figure 3 (see and one).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New purinergic receptor P2Y G-protein coupled 1 (P2RY1) gene polymorphic variants, useful e.g. in studying the expression and function of P2RY1 and screening candidate drugs for treating diseases related to P2RY1 activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56 NSSNIYLFNLSVSDLAFLCTLPMLIRSYAN-GNWIYGDVLCISNRYVLHANLYTSILFLT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGISVYMFNLALADFLYVLTLPALIFYYFNKTDWIFGDAMCKLQRFIFHVNLYGSILFLT 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115 FISIDRYLIIKYPFREHLLQKKEFAILISLAIWVLVTLELLPILPLINPVITDNGT-TCN 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 AM-NATCKNWLAA----EAALEK----YYLSIFYGIEFVVGVLGNTIVVYGYIFSLKNW 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWGNSTVASTAAVSSSFKCALTKTGFQFYYLPAVYILVFIIGFLGNSVAIWMFVFHMKPW 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a novel isolated polypeptide comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 23; Length 373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28.1%; Score 490.5; DB 23; Length : 36.0%; Pred. No. 2.7e-42; ive 60; Mismatches 125; Indels
                                                                                                                                  /note= "Wild type Val substituted by Gly"
                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure, Page -; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                    Tanguay DA;
                                                                                                                                                                                                                                                                                                                                                          (GENA-) GENAISSANCE PHARM INC.
                                                                                                                                                                                                                                                                      21-MAY-2001; 2001WO-US16432.
                                                                                                                                                                                                                                                                                                             19-MAY-2000; 2000US-205996P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 116; Conservative
    transgenic animal; human.
                                                                                                                                                                                                                                                                                                                                                                                                      Kazemi A, Koshy B,
                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-083074/11.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 373 AA;
                                                                                                             Misc-difference
                                                                                                                                                                               WO200190117-A2
                                                  Homo sapiens
                                                                                                                                                                                                                           29-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inverse agonists or partial agonists having applicability as therapeutic agents for treating diseases related to GPCR, e.g. lung cancer. Non-endogenous version of human GPCRs are of utilized in research settings and in vitro and in vivo system, incorporating GPCRs can be utilised to elucidate and understand the roles these receptors play in the human condition, both normal and diseased.
                                                                                                                                                                                                                                                                                                                       Human; gene therapy; G protein-coupled receptor; drug development; central nervous system disease; endocrine disease; metabolic disease; cancer; respiratory disease; digestive disease; immune disease;
Human kidney-originated G protein-coupled receptor protein encoded DNA, for developing drugs to treat central nervous
                                              N-PSDB; AAL43942.
                                                           WPI; 2002-566800/60.
                                                                                                                                                 18-JAN-2001; 2001JP-0010714.
30-MAR-2001; 2001JP-0102484.
                                                                                                                                                                                            17-JAN-2002; 2002WO-JP00270
                                                                                                                                                                                                                           25-JUL-2002
                                                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAO15399 standard; protein; 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                      WO200257441-A1
                                                                                                                                                                                                                                                                                                               inflammation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCTDEN-----IPLKMHYLPVIYGIIFLVGFPGNAVVISTYIFKMRPWKSSTIIMLNLAC 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFHILRVIRIESRLLS---ISCSIENQIHEAYIVSRPLAALNTFGNLLLYVVVSDNFQQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YSMCLTLLGFLIPLFVMCFFYYKIALFLKQRNRQVATALPLEKPLNLVIMAVVIFSVPFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFREHLLQKKEFAILISLAIWVLVTLELLPILPLINPVITDNGTTCNDFASSGDPNYNLI 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TDLLYLTSLPFLIHYYASGENWIFGDFMCKFIRFSFHFNLYSSILFLTCFSIFRYCVIIH 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PYHVMRNVRIASRLGSWKQYQCT-QVVINSFYIVTRPLAFLNSVINPVFYFLLGDHFRDM 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YNLILTATTFCLPLVIVTLCYTTI-IHTLTHGLQTDSCLK-QKARRLTILLLLAFYVCFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PMSCFSIHKTRCAVVACAVVWIISLVAVIPMTFLITSTNRTNRSACLDLTSSDELNTIKW
                                                                                                                                                                                                                                                                                                                                                                                       G protein-coupled receptor.
                                                                                                                    TAKEDA CHEM IND LTD.
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                                                                                       Ito T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         337 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                 infection; circulatory disease.
                                                                                       Shintani Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 477; DB 22;
Pred. No. 5.9e-41;
                                                                                       Miyajima
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 TGR30 and diseases,
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention comprises the amino acid and coding sequence of a human G protein-coupled receptor. The DNA and protein sequences of the invention are useful for developing drugs to prevent or treat (gene therapy): central nervous system diseases; endocrine diseases; metabolic diseases; cancer; respiratory diseases; digestive diseases; immune diseases; inflammations; infections; and circulatory diseases. The present amino acid sequence represents the human G protein-coupled receptor of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               endocrine diseases, metabolic diseases and cancer, including gene therapy \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 88-90;
313
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                                   306 LMNQLR 311
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                                                                                                      PYHVMRNVRIASRLGSWKQYQCT-QVVINSFYIVTRPLAFLNSVINPVFYFLLGDHFRDM 305
                                                                                                                                                                                                                                                                                                                                 SDLAFLCTLPMLIRSYANG-NWIYGDVLCISNRYVLHANLYTSILFLTFISIDRYLIIKY 126
                                                                                                                                                                                                                                                                                                                                                                              NCTDEN----IPLKMHYLPVIYGIIFLVGFPGNAVVISTYIFKMRPWKSSTIMLNLAC 77
VCSTVR
                                                                      PFHILRVIRIESRLLS---ISCSIENQIHEAYIVSRPLAALNTFGNLLLYVVVSDNFQQA 312
                                                                                                                                                                                      YSMCLTLLGFLIPLFVMCFFYYKIALFLKQRNRQVATALPLEKPLNLVIMAVVIFSVPFT 246
                                                                                                                                                                                                                                                             PFREHLLQKKEFAILISLAIWVLVTLELLPILPLINPVITDNGTTCNDFASSGDPNYNLI 186
                                                                                                                                                                                                                                                                                                    TDLLYLTSLPFLIHYYASGENWIFGDFMCKFIRFSFHFNLYSSILFLTCFSIFRYCVIIH 137
                                                                                                                                                                                                                           PMSCFSIHKTRCAVVACAVVWIISLVAVIPMTFLITSTNRTNRSACLDLTSSDELNTIKW 197
                                                                                                                                                 YNLILTATTECLELVIVTLCYTTI-IHTLTHGLQTDSCLK-QKARRLTILLLLAFYVCEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                           110;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27.3%; Score 477; DB 23; 35.9%; Pred. No. 5.9e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 337;
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